

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: University of Pittsburgh of the Commonwealth System
of Higher Education, 911 William Pitt Union
Pittsburgh, PA 15260

(ii) TITLE OF INVENTION: Gene Transfer For Treating a Connective Tissue
of a Mammalian Host

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Eckert Seamans Cherin & Mellott, LLC
(B) STREET: 600 Grant Street, 42nd Floor
(C) CITY: Pittsburgh
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 15219

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Meyers, Diane R.
(B) REGISTRATION NUMBER: 38,968
(C) REFERENCE/DOCKET NUMBER: 109070-11-1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (412) 566-6000
(B) TELEFAX: (412) 566-6099
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Human T-cell cDNA Library
- (B) CLONE: Human Interleukin-1 Receptor

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 55..1764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTCCTGAGA	AGCTGGACCC	CTTGGTAAAA	GACAAGGCCT	TCTCCAAGAA	GAAT	ATG	57
						Met	
						1	
AAA GTG TTA CTC AGA CTT ATT TGT TTC ATA GCT CTA CTG ATT TCT TCT							105
Lys Val Leu Leu Arg Leu Ile Cys Phe Ile Ala Leu Leu Ile Ser Ser							
	5		10			15	
CTG GAG GCT GAT AAA TGC AAG GAA CGT GAA GAA AAA ATA ATT TTA GTG							153
Leu Glu Ala Asp Lys Cys Lys Glu Arg Glu Glu Lys Ile Ile Leu Val							
	20		25			30	
TCA TCT GCA AAT GAA ATT GAT GTT CGT CCC TGT CCT CTT AAC CCA AAT							201
Ser Ser Ala Asn Glu Ile Asp Val Arg Pro Cys Pro Leu Asn Pro Asn							
	35		40			45	
GAA CAC AAA GGC ACT ATA ACT TGG TAT AAA GAT GAC AGC AAG ACA CCT							249
Glu His Lys Gly Thr Ile Thr Trp Tyr Lys Asp Asp Ser Lys Thr Pro							
	50		55			60	65
GTA TCT ACA GAA CAA GCC TCC AGG ATT CAT CAA CAC AAA GAG AAA CTT							297
Val Ser Thr Glu Gln Ala Ser Arg Ile His Gln His Lys Glu Lys Leu							
	70		75			80	
TGG TTT GTT CCT GCT AAG GTG GAG GAT TCA GGA CAT TAC TAT TGC GTG							345
Trp Phe Val Pro Ala Lys Val Glu Asp Ser Gly His Tyr Tyr Cys Val							
	85		90			95	
GTA AGA AAT TCA TCT TAC TGC CTC AGA ATT AAA ATA AGT GCA AAA TTT							393
Val Arg Asn Ser Ser Tyr Cys Leu Arg Ile Lys Ile Ser Ala Lys Phe							
	100		105			110	

00551775-170500

GAG Val	GAG Glu	AAT Asn	GAG Glu	CCT Pro	AAC Asn	TTA Leu	TGT Cys	TAT Tyr	AAT Asn	GCA Ala	GAA Ala	CCC Ala	ATA Ile	TTT Phe	AAG Lys	441
CAG Gln	AAA Lys	CTA Leu	CCC Pro	GTT Val	GCA Ala	GGA Gly	GAC Asp	GGA Gly	GGA Gly	CTT Leu	GTG Val	TGC Cys	CCT Pro	TAT Tyr	ATG Met	489
GAG Glu	TTT Phe	TTT Phe	AAA Lys	AAT Asn	GAA Glu	AAT Asn	AAT Asn	GAG Glu	TTA Leu	CCT Pro	AAA Lys	TTA Gln	CAG Gln	TGG Trp	TAT Tyr	537
AAG Lys	GAT Asp	TGC Cys	AAA Lys	CCT Pro	CTA Leu	CTT Leu	CTT Leu	GAC Asp	AAT Asn	ATA Ile	CAC His	Phs Phe	AGT Ser	GGA Gly	GTC Val	585
AAA Gln	GAT Asp	AGG Arg	CTC Leu	ATC Ile	GTG Val	ATG Met	AAT Asn	ATG Val	GCT Ala	GAA Glu	AAG Gln	CAT His	AGA Arg	GGG Gly	AAC Asn	633
TAT Tyr	ACT Thr	TGT Cys	CAT His	GCA Ala	TCC Ser	TAC Tyr	ACA Thr	TAC Tyr	TTG Leu	GGC Gly	AAG Gln	CAA Tyr	TAT Pro	CCT Pro	ATT Ile	681
ACC Thr	CGG Arg	GTA Val	ATA Ile	GAA Glu	TTT Phe	ATT Ile	ACT Thr	CTA Leu	GAG Glu	GAA Glu	AAA Asn	AAA Lys	CCC Pro	ACA Thr	AGG Arg	729
CCT Pro	GTG Val	ATT Ile	GTG Val	AGC Ser	CCA Pro	GCT Ala	AAT Asn	GAG Glu	ACA Thr	ATG Met	GAA Glu	GTA Val	GAC Asp	TTG Leu	GGA Gly	777
TCC Ser	CAG Gln	ATA Ile	CAA Gln	TTG Leu	ATC Ile	TGT Cys	AAT Asn	GTC Val	ACC Thr	GGC Gly	CAG Gln	TTG Leu	AGT Ser	GAC Asp	ATT Ile	825
GCT Ala	TAC Tyr	TGG Trp	AAG Lys	TGG Trp	AAT Asn	GGG Gly	TCA Ser	GTA Val	ATT Ile	GAT Asp	GAA Glu	GAT Asp	GAC Asp	CCA Pro	GTG Val	873
CTA Leu	GGG Gly	GAA Glu	GAC Asp	TAT Tyr	TAC Tyr	AGT Ser	GTG Val	GAA Glu	AAT Asn	CCT Pro	GCA Ala	AAC Asn	AAA Lys	AGA Arg	AGG Arg	921
AGT Ser	ACC Thr	CTC Leu	ATC Ile	ACA Thr	GTG Val	CTT Leu	AAT Asn	ATA Ile	TCG Ser	GAA Glu	ATT Ile	GAA Glu	AGT Ser	AGA Thr	TTT Phe	969
TAT Tyr	AAA Lys	CAT His	CCA Pro	TTT Phe	ACC Thr	TGT Cys	TTT Phe	GCC Ala	AAG Asn	AAT Asn	ACA Thr	CAT His	GGT Ser	ATA Ile	GAT Asp	1017
GCA Ala	GCA Ala	TAT Tyr	ATC Gln	CAG Gln	TTA Ile	ATA Ile	TAT Tyr	CCA Pro	GTC Val	ACT Thr	AAT Asn	TTC Phe	CAG Gln	CAC Thr	CAC His	1065
ATG Met	ATT Ile	GGT Gly	ATA Tyr	TGT Cys	GTC Val	TCG Thr	TTG Leu	ACA Thr	GTC Val	ATA Ile	ATT Ile	GTG Val	TGT Cys	TCT Ser	GTT Val	1113
TTC Phe	ATC Ile	TAT Tyr	AAA Lys	ATC Ile	TTC Phe	AGT Lys	AAT Ile	GAC Asp	ATT Ile	GTG Val	CTT Leu	TGG Trp	TAC Tyr	AGG Arg	GAT Asp	1161
TCC Ser	TGC Cys	TAT Tyr	GAT Asp	TTT Phe	CTC Leu	CCA Pro	ATA Ile	AAA Lys	GCT Ala	TCA Ser	GAT Asp	GGA Gly	AAG Lys	ACC Thr	TAT Tyr	1209

GAC GCA TAT ATA CTG TAT CCA AAG ACT GTT GGG GAA GGG TCT ACC TCT	1257
Asp Ala Tyr Ile Leu Tyr Pro Lys Thr Val Gly Glu Gly Ser Thr Ser	
390 395 400	
GAC TGT GAT ATT TTT GTG TTT AAA GTC TTG CCT GAG GTC TTG GAA AAA	1305
Asp Cys Asp Ile Phe Val Phe Lys Val Leu Pro Glu Val Leu Glu Lys	
405 410 415	
CAG TGT GGA TAT AAG CTG TTC ATT TAT GGA AGG GAT GAC TAC GTT GGG	1353
Gln Cys Gly Tyr Lys Leu Phe Ile Tyr Gly Arg Asp Tyr Val Gly	
420 425 430	
GAA GAC ATT GTT GAG GTC ATT AAT GAA AAC GTA AAG AAA AGC AGA AGA	1401
Glu Asp Ile Val Glu Val Ile Asn Glu Asn Val Lys Lys Ser Arg Arg	
435 440 445	
CTG ATT ATC ATT TTA GTC AGA GAA ACA TCA GGC TTC AGC TGG CTG GGT	1449
Leu Ile Ile Ile Leu Val Arg Glu Thr Ser Gly Phe Ser Trp Leu Gly	
450 455 460 465	
GGT TCA TCT GAA GAG CAA ATA GCC ATG TAT AAT GCT CTT GTT CAG GAT	1497
Gly Ser Ser Glu Glu Gln Ile Ala Met Tyr Asn Ala Leu Val Gln Asp	
470 475 480	
GGA ATT AAA GTT GTC CTG CTT GAG CTG GAG AAA ATC CAA GAC TAT GAG	1545
Gly Ile Lys Val Val Leu Leu Glu Leu Glu Lys Ile Gln Asp Tyr Glu	
485 490 495	
AAA ATG CCA GAA TCG ATT AAA TTC ATT AAG CAG AAA CAT GGG GCT ATC	1593
Lys Met Pro Glu Ser Ile Lys Phe Ile Lys Lys His Gly Ala Ile	
500 505 510	
CGC TGG TCA GGG GAC TTT ACA CAG GGA CCA CAG TCT GCA AAG ACA AGG	1641
Arg Trp Ser Gly Asp Phe Thr Gln Gly Pro Gln Ser Ala Lys Thr Arg	
515 520 525	
TTC TGG AAG AAT GTC AGG TAC CAC ATG CCA GTC CAG CGA CGG TCA CCT	1689
Phe Trp Lys Asn Val Arg Tyr His Met Pro Val Gln Arg Arg Ser Pro	
530 535 540 545	
TCA TCT AAA CAC CAG TTA CTG TCA CCA GCC ACT AAG GAG AAA CTG CAA	1737
Ser Ser Lys His Gln Leu Leu Ser Pro Ala Thr Lys Glu Lys Leu Gln	
550 555 560	
AGA GAG GCT CAC GTG CCT CTC GGG TAGCATGGA	1770
Arg Glu Ala His Val Pro Leu Gly	
565 570	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Val Leu Leu Arg Leu Ile Cys Phe Ile Ala Leu Leu Ile Ser
 1 5 10 15

Ser Leu Glu Ala Asp Lys Cys Lys Glu Arg Glu Glu Lys Ile Ile Leu
20 25 30

Val Ser Ser Ala Asn Glu Ile Asp Val Arg Pro Cys Pro Leu Asn Pro
35 40 45

Asn Glu His Lys Gly Thr Ile Thr Trp Tyr Lys Asp Asp Ser Lys Thr
50 55 60

Pro Val Ser Thr Glu Gln Ala Ser Arg Ile His Gln His Lys Glu Lys
65 70 75 80

Leu Trp Phe Val Pro Ala Lys Val Glu Asp Ser Gly His Tyr Tyr Cys
85 90 95

Val Val Arg Asn Ser Ser Tyr Cys Leu Arg Ile Lys Ile Ser Ala Lys
100 105 110

Phe Val Glu Asn Glu Pro Asn Leu Cys Tyr Asn Ala Gln Ala Ile Phe
115 120 125

Lys Gln Lys Leu Pro Val Ala Gly Asp Gly Gly Leu Val Cys Pro Tyr
130 135 140

Met Glu Phe Phe Lys Asn Glu Asn Asn Glu Leu Pro Lys Leu Gln Trp
145 150 155 160

Tyr Lys Asp Cys Lys Pro Leu Leu Leu Asp Asn Ile His Phe Ser Gly
165 170 175

Val Lys Asp Arg Leu Ile Val Met Asn Val Ala Glu Lys His Arg Gly
180 185 190

Asn Tyr Thr Cys His Ala Ser Tyr Thr Tyr Leu Gly Lys Gln Tyr Pro
195 200 205

Ile Thr Arg Val Ile Glu Phe Ile Thr Leu Glu Glu Asn Lys Pro Thr
210 215 220

Arg Pro Val Ile Val Ser Pro Ala Asn Glu Thr Met Glu Val Asp Leu
225 230 235 240

Gly Ser Gln Ile Gln Leu Ile Cys Asn Val Thr Gly Gln Leu Ser Asp
245 250 255

Ile Ala Tyr Trp Lys Trp Asn Gly Ser Val Ile Asp Glu Asp Asp Pro
260 265 270

Val Leu Gly Glu Asp Tyr Tyr Ser Val Glu Asn Pro Ala Asn Lys Arg
275 280 285

00734736 120500

Arg Ser Thr Leu Ile Thr Val Leu Asn Ile Ser Glu Ile Glu Ser Arg
290 295 300

Phe Tyr Lys His Pro Phe Thr Cys Phe Ala Lys Asn Thr His Gly Ile
305 310 315 320

Asp Ala Ala Tyr Ile Gln Leu Ile Tyr Pro Val Thr Asn Phe Gln Lys
325 330 335

His Met Ile Gly Ile Cys Val Thr Leu Thr Val Ile Ile Val Cys Ser
340 345 350

Val Phe Ile Tyr Lys Ile Phe Lys Ile Asp Ile Val Leu Trp Tyr Arg
355 360 365

Asp Ser Cys Tyr Asp Phe Leu Pro Ile Lys Ala Ser Asp Gly Lys Thr
370 375 380

Tyr Asp Ala Tyr Ile Leu Tyr Pro Lys Thr Val Gly Glu Gly Ser Thr
385 390 395 400

Ser Asp Cys Asp Ile Phe Val Phe Lys Val Leu Pro Glu Val Leu Glu
405 410 415

Lys Gln Cys Gly Tyr Lys Leu Phe Ile Tyr Gly Arg Asp Asp Tyr Val
420 425 430

Gly Glu Asp Ile Val Glu Val Ile Asn Glu Asn Val Lys Lys Ser Arg
435 440 445

Arg Leu Ile Ile Ile Leu Val Arg Glu Thr Ser Gly Phe Ser Trp Leu
450 455 460

Gly Gly Ser Ser Glu Glu Gln Ile Ala Met Tyr Asn Ala Leu Val Gln
465 470 475 480

Asp Gly Ile Lys Val Val Leu Leu Glu Leu Glu Lys Ile Gln Asp Tyr
485 490 495

Glu Lys Met Pro Glu Ser Ile Lys Phe Ile Lys Gln Lys His Gly Ala
500 505 510

Ile Arg Trp Ser Gly Asp Phe Thr Gln Gly Pro Gln Ser Ala Lys Thr
515 520 525

Arg Phe Trp Lys Asn Val Arg Tyr His Met Pro Val Gln Arg Arg Ser
530 535 540

Pro Ser Ser Lys His Gln Leu Leu Ser Pro Ala Thr Lys Glu Lys Leu
545 550 555 560

Gln Arg Glu Ala His Val Pro Leu Gly
565

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Mouse T-cell cDNA Library
- (B) CLONE: Mouse Interleukin-1 Receptor

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 46..1776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGATGTCATC AGAGTTCCCA GTGCCCCGAA CCGTGAACAA CACAA	ATG GAG AAT	54
	Met Glu Asn	
	1	
ATG AAA GTG CTA CTG GGG CTC ATT TGT CTC ATG GTG CCT CTG CTG TCG		102
Met Lys Val Leu Leu Gly Leu Ile Cys Leu Met Val Pro Leu Leu Ser		
5	15	
CTG GAG ATT GAC GTA TGT ACA GAA TAT CCA AAT CAG ATC GTT TTG TTT		150
Leu Glu Ile Asp Val Cys Thr Glu Tyr Pro Asn Gln Ile Val Leu Phe		
20	25	30
TTA TCT GTA AAT GAA ATT GAT ATT CGC AAG TGT CCT CTT ACT CCA AAT		198
Leu Ser Val Asn Glu Ile Asp Ile Arg Lys Cys Pro Leu Thr Pro Asn		
40	45	50
AAA ATG CAC GGC GAC ACC ATA ATT TGG TAC AAG AAT GAC AGC AAG ACC		246
Lys Met His Gly Asp Thr Ile Ile Trp Tyr Lys Asn Asp Ser Lys Thr		
55	60	65
CCC ATA TCA GCG GAC CGG GAC TCC AGG ATT CAT CAG CAG AAT GAA CAT		294
Pro Ile Ser Ala Asp Arg Asp Ser Arg Ile His Gln Gln Asn Glu His		
70	75	80

CTT TGG TTT GTA CCT GCC AAG GTG GAG GAC TCA GGA TAT TAC TAT TGT Leu Trp Phe Val Pro Ala Lys Val Glu Asp Ser Gly Tyr Tyr Tyr Cys	342
85	
ATA GTA AGA AAC TCA ACT TAC TGC CTC AAA ACT AAA GTA ACC GTA ACT Ile Val Arg Asn Ser Thr Tyr Cys Leu Lys Thr Lys Val Thr Val Thr	390
100 105 110 115	
GTG TTA GAG AAT GAC CCT GGC TTG TGT TAC AGC ACA CAG GCC ACC TTC Val Leu Glu Asn Asp Pro Gly Leu Cys Tyr Ser Thr Gln Ala Thr Phe	438
120 125 130	
CCA CAG CGG CTC CAC ATT GCC GGG GAT GGA AGT CTT GTG TGC CCT TAT Pro Gln Arg Leu His Ile Ala Gly Asp Gly Ser Leu Val Cys Pro Tyr	486
135 140 145	
GTG ACT TAT TTT AAA GAT GAA AAT GAG TTA CCC GAG GTC CAG TGG Val Ser Tyr Phe Lys Asp Glu Asn Asn Glu Leu Pro Glu Val Gln Trp	534
150 155 160	
TAT AAG AAC TGT AAA CCT CTG CTT GAC AAC GTG AGC TTC TTC GGA Tyr Lys Asn Cys Lys Pro Leu Leu Asp Asn Val Ser Phe Phe Gly	582
165 170 175	
GTA AAA GAT AAA CTG TTG GTG AGG AAT GTG GCT GAA GAG CAC AGA GGG Val Lys Asp Lys Leu Leu Val Arg Asn Val Ala Glu Glu His Arg Gly	630
180 185 190 195	
GAC TAT ATA TGC CGT ATG TCC TAT ACG TTC CGG GGG AAG CAA TAT CCG Asp Tyr Ile Cys Arg Met Ser Tyr Thr Thr Arg Gly Lys Gln Tyr Pro	678
200 205 210	
GTC ACA CGA GTA ATA CAA TTT ATC ACA ATA GAT GAA AAC AAG AGG GAC Val Thr Arg Val Ile Gln Phe Ile Thr Thr Ile Asp Glu Asn Lys Arg Asp	726
215 220 225	
AGA CCT GTT ATC CTG AGC CCT CGG AAT GAG ACG ATC GAA GCT GAC CCA Arg Pro Val Ile Leu Ser Pro Arg Asn Glu Thr Ile Glu Ala Asp Pro	774
230 235 240	
GGA TCA ATG ATA CAA CTG ATC TGC AAC GTC ACG GGC CAG TTC TCA GAC Gly Ser Met Ile Gln Leu Ile Cys Asn Val Thr Gly Lys Phe Ser Asp	822
245 250 255	
CTT GTC TAC TGG AAG TGG AAT GGA TCA GAA ATT GAA TGG AAT GAT CCA Leu Val Tyr Trp Lys Trp Asn Gly Ser Glu Ile Glu Trp Asn Asp Pro	870
260 265 270 275	
TTT CTA GCT GAA GAC TAT CAA TTT GTG GAA CAT CCT TCA ACC AAA AGA Phe Leu Ala Glu Asp Tyr Gln Phe Val Glu His Pro Ser Thr Lys Arg	918
280 285 290	
AAA TAC ACA CTC ATT ACA ACA CTT AAC ATT TCA GAA GTT AAA AGC CAG Lys Tyr Thr Thr Ile Thr Thr Leu Asn Ile Ser Glu Val Lys Ser Gln	966
295 300 305	
TTT TAT CGC TAT CCG TTT ATC TGT GTT GTT AAG AAC ACA AAT ATT TTT Phe Tyr Arg Tyr Pro Phe Ile Cys Val Val Lys Asn Thr Asn Ile Phe	1014
310 315 320	
GAC TCG GCG CAT GTG CAG TTA ATA TAC CCA GTC CCT GAC TTC AAG AAT Glu Ser Ala His Val Gln Leu Ile Tyr Pro Val Val Asp Phe Lys Asn	1062
325 330 335	
TAC CTC ATC GGG GGC TTT ATC ATC CTC ACG GCT ACA ATT GTA TGC TGT Tyr Leu Ile Gly Gly Phe Ile Ile Leu Thr Thr Ala Thr Ile Val Cys Cys	1110
340 345 350 355	

001115-10500

GTG TGC ATC TAT AAA GTC TTC AAG GTT GAC ATA GTG CTT TGG TAC AGG Val Cys Ile Tyr Lys Val Phe Lys Val Asp Ile Val Leu Trp Tyr Arg 360 365	1158
GAC TCC TGC TCT GGT TTT CTT CCT TCA AAA GCT TCA GAT GGA AAG ACA Asp Ser Cys Ser Gly Phe Leu Pro Ser Lys Ala Ser Asp Gly Lys Thr 375 380 385	1206
TAC GAT GCA TAT ATT CTT TAT CCC AAG ACC CTG GGA GAG GGG TCC TTC Tyr Asp Ala Tyr Ile Leu Tyr Pro Lys Thr Leu Gly Glu Gly Ser Phe 390 395 400	1254
TCA GAC TTA GAT ACT TTT GTT TTT AAA CTG TTG CCT GAG GTC TTG GAG Ser Asp Leu Asp Thr Phe Val Phe Lys Leu Leu Pro Glu Val Leu Glu 405 410 415	1302
GGA CAG TTT GGA TAC AAG CTG TTC ATT TAT GGA AGG GAT GAC TAT GTT Gly Gln Phe Gly Tyr Lys Leu Phe Ile Tyr Gly Arg Asp Asp Tyr Val 420 425 430 435	1350
GGA GAA GAT ACC ATC GAG GTT ACT AAT GAA AAT GTA AAG AAA AGC AGG Gly Glu Asp Thr Ile Glu Val Thr Asn Glu Asn Val Lys Lys Ser Arg 440 445 450	1398
AGG CTG ATT ATC ATT CTA GTG AGA GAT ATG GGA GGC TTC AGC TGG CTG Arg Leu Ile Ile Ile Leu Val Arg Asp Met Gly Gly Phe Ser Trp Leu 455 460 465	1446
GGC CAG TCA TCT GAA GAG CAA ATA GCC ATA TAC AAT GCT CTC ATC CAG Gly Gln Ser Ser Glu Glu Gln Ile Ala Ile Tyr Asn Ala Leu Ile Gln 470 475 480	1494
GAA GGA ATT AAA ATC GTC CTG CTT GAG TTG GAG AAA ATC CAA GAC TAT Glu Gly Ile Lys Ile Val Leu Leu Glu Leu Glu Lys Ile Gln Asp Tyr 485 490 495	1542
GAG AAA ATG CCA GAT TCT ATT CAG TTC ATT AAG CAG AAA CAC GGA GTC Glu Lys Met Pro Asp Ser Ile Gln Phe Ile Lys Gln Lys His Gly Val 500 505 510 515	1590
ATT TGC TGG TCA GGA GAC TTT CAA GAA AGA CCA CAG TCT GCA AAG ACC Ile Cys Trp Ser Gly Asp Phe Gln Glu Arg Pro Gln Ser Ala Lys Thr 520 525 530	1638
AGG TTC TGG AAA AAC TTA AGA TAC CAG ATG CCA GCC CAA CGG AGA TCA Arg Phe Trp Lys Asn Leu Arg Tyr Gln Met Pro Ala Gln Arg Arg Ser 535 540 545	1686
CCA TTG TCT AAA CAC CGC TTA CTA ACC CTG GAT CCT GTG CGG GAC ACT Pro Leu Ser Lys His Arg Leu Leu Thr Leu Asp Pro Val Arg Asp Thr 550 555 560	1734
AAG GAG AAA CTG CCG GCA GCA ACA CAC TTA CCA CTC GGC TAGCATGGC Lys Glu Lys Leu Pro Ala Ala Thr His Leu Pro Leu Gly 565 570 575	1782

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Asn Met Lys Val Leu Leu Gly Leu Ile Cys Leu Met Val Pro
 1 5 10 15

Leu Leu Ser Leu Glu Ile Asp Val Cys Thr Glu Tyr Pro Asn Gln Ile
 20 25 30

Val Leu Phe Leu Ser Val Asn Glu Ile Asp Ile Arg Lys Cys Pro Leu
 35 40 45

Thr Pro Asn Lys Met His Gly Asp Thr Ile Ile Trp Tyr Lys Asn Asp
 50 55 60

Ser Lys Thr Pro Ile Ser Ala Asp Arg Asp Ser Arg Ile His Gln Gln
 65 70 75 80

Asn Glu His Leu Trp Phe Val Pro Ala Lys Val Glu Asp Ser Gly Tyr
 85 90 95

Tyr Tyr Cys Ile Val Arg Asn Ser Thr Tyr Cys Leu Lys Thr Lys Val
 100 105 110

Thr Val Thr Val Leu Glu Asn Asp Pro Gly Leu Cys Tyr Ser Thr Gln
 115 120 125

Ala Thr Phe Pro Gln Arg Leu His Ile Ala Gly Asp Gly Ser Leu Val
 130 135 140

Cys Pro Tyr Val Ser Tyr Phe Lys Asp Glu Asn Asn Glu Leu Pro Glu
 145 150 155 160

Val Gln Trp Tyr Lys Asn Cys Lys Pro Leu Leu Leu Asp Asn Val Ser
 165 170 175

Phe Phe Gly Val Lys Asp Lys Leu Leu Val Arg Asn Val Ala Glu Glu
 180 185 190

His Arg Gly Asp Tyr Ile Cys Arg Met Ser Tyr Thr Phe Arg Gly Lys
 195 200 205

Gln Tyr Pro Val Thr Arg Val Ile Gln Phe Ile Thr Ile Asp Glu Asn
 210 215 220

Lys Arg Asp Arg Pro Val Ile Leu Ser Pro Arg Asn Glu Thr Ile Glu
 225 230 235 240

Ala Asp Pro Gly Ser Met Ile Gln Leu Ile Cys Asn Val Thr Gly Gln
 245 250 255

00734475.120600

Phe Ser Asp Leu Val Tyr Trp Lys Trp Asn Gly Ser Glu Ile Glu Trp
260 265 270

Asn Asp Pro Phe Leu Ala Glu Asp Tyr Gln Phe Val Glu His Pro Ser
275 280 285

Thr Lys Arg Lys Tyr Thr Leu Ile Thr Thr Leu Asn Ile Ser Glu Val
290 295 300

Lys Ser Gln Phe Tyr Arg Tyr Pro Phe Ile Cys Val Val Lys Asn Thr
305 310 315 320

Asn Ile Phe Glu Ser Ala His Val Gln Leu Ile Tyr Pro Val Pro Asp
325 330 335

Phe Lys Asn Tyr Leu Ile Gly Gly Phe Ile Ile Leu Thr Ala Thr Ile
340 345 350

Val Cys Cys Val Cys Ile Tyr Lys Val Phe Lys Val Asp Ile Val Leu
355 360 365

Trp Tyr Arg Asp Ser Cys Ser Gly Phe Leu Pro Ser Lys Ala Ser Asp
370 375 380

Gly Lys Thr Tyr Asp Ala Tyr Ile Leu Tyr Pro Lys Thr Leu Gly Glu
385 390 395 400

Gly Ser Phe Ser Asp Leu Asp Thr Phe Val Phe Lys Leu Leu Pro Glu
405 410 415

Val Leu Glu Gly Gln Phe Gly Tyr Lys Leu Phe Ile Tyr Gly Arg Asp
420 425 430

Asp Tyr Val Gly Glu Asp Thr Ile Glu Val Thr Asn Glu Asn Val Lys
435 440 445

Lys Ser Arg Arg Leu Ile Ile Ile Leu Val Arg Asp Met Gly Gly Phe
450 455 460

Ser Trp Leu Gly Gln Ser Ser Glu Glu Gln Ile Ala Ile Tyr Asn Ala
465 470 475 480

Leu Ile Gln Glu Gly Ile Lys Ile Val Leu Leu Glu Leu Glu Lys Ile
485 490 495

Gln Asp Tyr Glu Lys Met Pro Asp Ser Ile Gln Phe Ile Lys Gln Lys
500 505 510

His Gly Val Ile Cys Trp Ser Gly Asp Phe Gln Glu Arg Pro Gln Ser
515 520 525

Ala Lys Thr Arg Phe Trp Lys Asn Leu Arg Tyr Gln Met Pro Ala Gln
530 535 540

Arg Arg Ser Pro Leu Ser Lys His Arg Leu Leu Thr Leu Asp³ Pro Val
545 550 555 560

Arg Asp Thr Lys Glu Lys Leu Pro Ala Ala Thr His Leu Pro Leu Gly
565 570 575

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Primer Oligonucleotide to 5'Leader Sequence of
IL-1 Receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGATCCCC TCCTGAGAAG CT

22

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Primer Oligonucleotide Upstream of
Transmembrane Portion of

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGGATCCCA TGTGCTACTG G

21

005021.5.120500